CLAIM AMENDMENTS

1. (currently amended) A method of detecting and identifying an orthopoxvirus within a sample comprising:

adding to the sample reagents for nucleic acid amplification and at least one pair of primers capable of amplifying at least one region of the orthopoxvirus genome, said pair of primers being selected from the group consisting of 12 or more consecutive nucleotides of ATGCCGGTACTTATGTATGTGC (SPOXHA5, SEQ ID NO: 1) and 12 or more consecutive nucleotides of TCTTGTCTGTTGTGGATTCT (SPOXHA3, SEQ ID NO: 2) when said region of the orthopoxvirus genome is gene HA; and 12 or more consecutive nucleotides of TACCGGTCTCAGCGAATC (SPOXcrmB5, SEQ ID NO: 3) and 12 or more consecutive nucleotides of ACCGTCTCCGAATGCGGCAT (SPOXcrmB3, SEQ ID NO: 4) when said region of the orthopoxvirus genome is gene crmB; ~~and said region of the orthopoxvirus genome selected from the group consisting of HA and crmB;~~

incubating the sample under conditions suitable for nucleic acid amplification thereby producing an amplicon if the sample contains orthopoxvirus;

adding at least one restriction enzyme selected from the group consisting of: Sau 3AI, Spe I, Dra I, Hpa I, Ssp I, Alw 44I, Nla III, and combinations thereof; and

determining if restriction enzyme digestion of an amplicon has occurred.

2. (original) The method according to claim 1 wherein restriction enzyme digestion of an amplicon is determined by gel electrophoresis.

3. cancelled

4. cancelled

5. cancelled

6. cancelled

7. cancelled

8. cancelled

9. (new) The method according to claim 1 wherein the orthopoxvirus is identified based on the restriction enzyme digestion pattern.